



SEQUENCE LISTING

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SEP 30 2003  
TECH CENTER 1600/2300

- <110> Behan, Dominic P.  
Chalmers, Derek T.  
Lin, I-Lin  
Liaw, Chen W.  
Lehman-Bruinsma, Karin  
Lowitz, Kevin P.  
Dang, Huong T.  
Chen, Ruoping  
Gore, Martin  
White, Carol
- <120> Non-Endogenous Constitutively Activated Human G Protein Coupled Receptors
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Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe  
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Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met  
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Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met  
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Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe  
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Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser  
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Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys  
 195 200 205

Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser  
 210 215 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln  
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Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu  
 245 250 255

Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn  
 260 265 270

Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala

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Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile  
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Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe  
 305 310 315 320

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val  
 325 330 335

Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile  
 340 345 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro  
 355 360 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp  
 370 375 380

Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr  
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Thr Val Val

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 35 40 45

Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu  
 50 55 60

Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser  
 65 70 75 80

Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr  
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Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu  
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Met Leu Ile Asn Val Asp Arg Tyr Ala Ala Ile Val His Pro Leu Arg

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Leu Arg His Leu Arg Arg Pro Arg Val Ala Arg Leu Leu Cys Leu Gly  
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 145 150 155 160

Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe  
 165 170 175

Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val  
 180 185 190

Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val  
 195 200 205

Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr  
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Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu  
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Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val  
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Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg  
 260 265 270

Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala  
 275 280 285

Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe  
 290 295 300

Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser  
 305 310 315 320

Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala  
 325 330 335

Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu  
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Arg Pro Ser Asp Ser His Ser Leu Ser Ser Phe Thr Gln Cys Pro Gln

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Gly Ala Leu	Leu Val Val Val	Leu Arg Thr Pro Gly	Leu Arg Asp Ala
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Leu Tyr Leu	Ala His Leu Cys Val Val	Asp Leu Leu Ala Ala	Ala Ser
50		55	60
Ile Met Pro	Leu Gly Leu Leu Ala Ala	Pro Pro Pro Gly	Leu Gly Arg
65		70	75
Val Arg Leu	Gly Pro Ala Pro Cys Arg	Ala Ala Arg Phe	Leu Ser Ala
	85	90	95
Ala Leu Leu	Pro Ala Cys Thr Leu	Gly Val Ala Ala	Leu Gly Leu Ala
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Arg Tyr Arg	Leu Ile Val His Pro	Leu Arg Pro Gly	Ser Arg Pro Pro
	115	120	125
Pro Val Leu	Val Leu Thr Ala Val	Trp Ala Ala Ala	Gly Leu Leu Gly
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Ala Leu Ser	Leu Leu Gly Pro Pro	Pro Pro Pro Ala	Pro Pro Ala
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Arg Cys Ser	Val Leu Ala Gly Gly	Leu Gly Pro Phe	Arg Pro Leu Trp
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Ala Leu Leu	Ala Phe Ala Leu Pro	Ala Leu Leu Leu	Gly Ala Tyr
	180	185	190
Gly Gly Ile	Phe Val Val Ala Arg	Arg Ala Ala Leu	Arg Pro Pro Arg
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Pro Ala Arg	Gly Ser Arg Leu Arg	Ser Asp Ser Leu	Asp Ser Arg Leu
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Ser Ile Leu	Pro Pro Leu Arg Pro	Arg Leu Pro Gly	Gly Lys Ala Ala
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Leu Ala Pro	Ala Leu Ala Val Gly	Gln Phe Ala Ala	Cys Trp Leu Pro

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Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu  
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Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe  
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Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu  
 290 295 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala  
 305 310 315 320

Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly  
 325 330 335

Pro Ala Val Gly Pro Ser Glu Ala Pro Glu Gln Thr Pro Glu Leu Ala  
 340 345 350

Gly Gly Arg Ser Pro Ala Tyr Gln Gly Pro Pro Glu Ser Ser Leu Ser  
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&lt;211&gt; 1008

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

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Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala  
 35 40 45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp  
 50 55 60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu  
 65 70 75 80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val  
 85 90 95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg  
 100 105 110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly  
 115 120 125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro  
 130 135 140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val  
 145 150 155 160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro

165

170

175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala  
 180 185 190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met  
 195 200 205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu  
 210 215 220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro  
 225 230 235 240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu  
 245 250 255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
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Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
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&lt;210&gt; 9

&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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<400> 10

Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly His Arg Pro  
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Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp  
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Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly  
 35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr  
 50 55 60

Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe  
 65 70 75 80

Leu Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His  
 85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly  
 100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp  
 115 120 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro  
 130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr  
 145 150 155 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp  
 165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser  
 180 185 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu  
 195 200 205

Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln  
 210 215 220

Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile  
 225 230 235 240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu  
 245 250 255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
 260 265 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
 275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
 290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
 305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
 325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
 340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
 355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
 370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
 385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
 405 410 415

Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser  
 420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala  
 435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly  
 450 455 460

Ala Gly Pro Thr  
 465

<210> 11

<211> 1248

<212> DNA

<213> Homo sapiens

<400> 11

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cgcagccact	tcttctctcc	cgtgtctgtg	gtgtatgtgc	caatttttgt	ggtgggggtc	180
attggcaatg	tcctggtgtg	cctggtgatt	ctgcagcacc	aggctatgaa	gacgccacc	240
aactactacc	tcttcagcct	ggcgggtctct	gacctcctgg	tcctgctcct	tggaatgcc	300

ctggaggtct atgagatgtg gcgcaactac cctttcttgt tcgggcccgt gggctgctac 360  
 ttcaagacgg ccctctttga gaccgtgtgc ttgcctcca tcctcagcat caccaccgtc 420  
 agcgtggagc gctacgtggc catctacac ccgttccgcg ccaaactgca gagcaccggg 480  
 cgccggggccc tcaggatcct cggcatcgtc tggggcttct ccgtgctctt ctccctgccc 540  
 aacaccagca tccatggcat caagttccac tacttcccca atgggtccct ggtcccaggt 600  
 tcggccacct gtacggtcac caagcccatg tggatctaca atttcatcat ccaggtcacc 660  
 tccttcctat tctacctct ccccatgact gtcatcagtg tcctctacta cctcatggca 720  
 ctcagactaa agaaagacaa atctcttgag gcagatgaag ggaatgcaaa tattcaaaga 780  
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<210> 12  
 <211> 415  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln  
 1 5 10 15

Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr  
 20 25 30

Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val  
 35 40 45

Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val  
 50 55 60

Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr  
 65 70 75 80



Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu  
 85 90 95

Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe  
 100 105 110

Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr  
 115 120 125

Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg  
 130 135 140

Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg  
 145 150 155 160

Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu  
 165 170 175

Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe  
 180 185 190

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
 195 200 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
 210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
 225 230 235 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
 245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val  
 260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg  
 275 280 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val  
 290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser  
 305 310 315 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala  
 325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln  
 340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu  
 355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys  
 370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
 385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
 405 410 415

<210> 13  
 <211> 1173  
 <212> DNA  
 <213> Homo sapiens

<400> 13  
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 gattttggaa aggaaatctg tgtatTTTtg ctactactg actatctgtt atgtacagca 300  
 tctgtatata acattgtcct catcagctat gatcgatacc tgtcagtctc aaatgctgtg 360  
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 tccaacatct gtggacactc attcagaggt agactatctt caaggagatc tctttctgca 720  
 tcgacagaag ttctgcatc ctttcattca gagagacaga ggagaaagag tagtctcatg 780  
 ttttctcaa gaaccaagat gaatagcaat acaattgctt ccaaaatggg ttccttctcc 840  
 caatcagatt ctgtagctct tcaccaaagg gaacatgttg aactgcttag agccaggaga 900

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 agaattgcat tttggcttca gtgggttcaat tcctttgtca atcctctttt gtatccattg 1080  
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 ccatcacaac acagtcgggc agtatcttct taa 1173

<210> 14  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens

<400> 14

Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val  
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Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly  
 20 25 30

Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His  
 35 40 45

Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val  
 50 55 60

Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp  
 65 70 75 80

Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu  
 85 90 95

Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg  
 100 105 110

Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly  
 115 120 125

Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe  
 130 135 140

Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu  
 145 150 155 160

Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala

165

170

175

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr  
 180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser  
 195 200 205

Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys  
 210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala  
 225 230 235 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys  
 245 250 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile  
 260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His  
 275 280 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser  
 290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser  
 305 310 315 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys  
 325 330 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe  
 340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala  
 355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His  
 370 375 380

Ser Arg Ser Val Ser Ser  
 385 390

&lt;210&gt; 15

<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 15  
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30

<210> 16  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 16  
ctgggatcct acgagagcat ttttcacaca g

31

<210> 17  
<211> 1128  
<212> DNA  
<213> Homo sapiens

<400> 17  
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aagctggcca cgctcagcct gctgctgtgc gtgagcctag cgggcaacgt gctgttcgcg 120  
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<210> 18  
 <211> 375  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala  
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Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser  
 20 25 30

Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser  
 35 40 45

Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp  
 50 55 60

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg  
 65 70 75 80

Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys  
 85 90 95

Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu  
 100 105 110

Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg  
 115 120 125

Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val  
 130 135 140

Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Phe Pro Pro Val Leu  
 145 150 155 160

Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg  
 165 170 175

Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val

180

185

190

Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile  
 195 200 205

His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser  
 210 215 220

His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala  
 225 230 235 240

Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val  
 245 250 255

Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val  
 260 265 270

Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala  
 275 280 285

Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser  
 290 295 300

Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu  
 305 310 315 320

Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val  
 325 330 335

Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln  
 340 345 350

Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys  
 355 360 365

Asp Leu Lys Gly Ile Gly Leu  
 370 375

&lt;210&gt; 19

&lt;211&gt; 1002

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

atgaacacca cagtgatgca aggccttcaac agatctgagc ggtgccccag agacactcgg 60

atagtacagc tgggtattccc agccctctac acagtgggtt tcttgaccgg catcctgctg 120

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aatacttttg ctctgtgggt gtttgttcac atccccagct cctccacctt catcatctac 180
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tctgactcac acctggcacc ctggcagctc agagcttttg tgtgtcgttt ttcttcggtg 300
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ttcctcaaga tcatcagacc ttgagaaat atttttctaa aaaaacctgt ttttgcaaaa 420
acggtctcaa tcttcactcg gttctttttg ttcttcactt ccctgccaaa tacgatcttg 480
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tccaaaagta aggacagaaa aaacaacaaa aagctggaag gcaaagtatt tgttgtcgtg 720
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caaaccaaca ataagactga ctgtagactg caaaatcaac tgtttattgc taaagaaaca 840
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aaaaaattca cagaaaagct accatgtatg caagggagaa agaccacagc atcaagccaa 960
gaaaatcata gcagtcagac agacaacata acctagggt ga 1002

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<210> 20
<211> 333
<212> PRT
<213> Homo sapiens

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<400> 20

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Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1          5          10          15

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```

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
20          25          30

```

```

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
35          40          45

```

```

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
50          55          60

```

```

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
65          70          75          80

```

```

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg

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85

90

95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu  
 100 105 110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu  
 115 120 125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile  
 130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu  
 145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu  
 165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys  
 180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val  
 195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys  
 210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val  
 225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro  
 245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn  
 260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn  
 275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr  
 290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln  
 305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly

<210> 21  
 <211> 1122  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
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 gccatcttgt ccctgctggg gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180  
 ctgctggacc tgtgcctggc cgatggcata cgctctgccg tctgcttccc ctttgtgctg 240  
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 tttatggcgg tgctcttttg cttccatgcg gccttcatgc tgttctgcat cagcgtcacc 360  
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 gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt 480  
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 ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc 600  
 catgctgtct acggcaagct gctcctcttc gattatcgtc accgcaagat gaagccagtg 660  
 cagatggtgc cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag 720  
 gctgctgcca actggatcgc cggctttggc cgtgggcccc tgccaccaac cctgctgggt 780  
 atccggcaga atgggcatgc agccagccgg cggctactgg gcattggacga ggtcaagggt 840  
 gaaaagcagc tgggcccgcg gttctacgcg atcacactgc tctttctgct cctctgggtca 900  
 ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gccccaccgc 960  
 tacctggcca ctgctgtttg gatgagcttc gccaggctg ccgtcaacct aattgtctgc 1020  
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 ggaggtgccc cggtcccag agaaccctac tgtgtcatgt ga 1122

<210> 22  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser  
 1 5 10 15

Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile

20

25

30

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu  
 35 40 45

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu  
 50 55 60

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu  
 65 70 75 80

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys  
 85 90 95

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe  
 100 105 110

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His  
 115 120 125

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile  
 130 135 140

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe  
 145 150 155 160

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe  
 165 170 175

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met  
 180 185 190

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu  
 195 200 205

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro  
 210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln  
 225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro  
 245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu

260

265

270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe  
 275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val  
 290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg  
 305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn  
 325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr  
 340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu  
 355 360 365

Pro Tyr Cys Val Met  
 370

<210> 23

<211> 1053

<212> DNA

<213> Homo sapiens

<400> 23

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acttatgact acagtcaata tgaattgata tgtatcaaag aagatgtcag agaatttgca	120
aaagttttcc tccctgtatt cctcacaata gctttcgtca ttggacttgc aggcaattcc	180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaacaga tgtgtacatc	240
ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcctttttg ggctgttaat	300
gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca	360
ctaaactttg tctctggaat gcagtttctg gcttgcatca gcatagacag atatgtggca	420
gtaactaatg tcccagcca atcaggagtg ggaaaacat gctggatcat ctgtttctgt	480
gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaataac	540
aatgctaggt gcattcccat tttccccgc tacctaggaa catcaatgaa agcattgatt	600
caaatgctag agatctgcat tggatttgta gtacctttc ttattatggg ggtgtgctac	660
tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa	720

gttctgctca cagtcggttat agtttttcatt gtcactcaac tgccttataa cattgtcaag 780  
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 atggacatcg ccatccaagt cacagaaagc attgcactct ttcacagctg cctcaaccca 900  
 atccttttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960  
 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020  
 cctacagagc caaccagtac ttttagcatt taa 1053

<210> 24  
 <211> 350  
 <212> PRT  
 <213> Homo sapiens

<400> 24

Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn  
 1 5 10 15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile  
 20 25 30

Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu  
 35 40 45

Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala  
 50 55 60

Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile  
 65 70 75 80

Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Phe Thr Leu Pro Phe  
 85 90 95

Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys  
 100 105 110

Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln  
 115 120 125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val  
 130 135 140

Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys  
 145 150 155 160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr  
 165 170 175  
 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu  
 180 185 190  
 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly  
 195 200 205  
 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala  
 210 215 220  
 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys  
 225 230 235 240  
 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr  
 245 250 255  
 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile  
 260 265 270  
 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr  
 275 280 285  
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val  
 290 295 300  
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys  
 305 310 315 320  
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe  
 325 330 335  
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile  
 340 345 350

<210> 25  
 <211> 1116  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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 agcgcggtgt gcacgctggg ggtgccggcc aactgcctga ctgcgtggct ggcgctgctg 180

caggtactgc agggcaacgt gctggcgcgtc tacctgctct gcctggcact ctgcgaactg 240  
 ctgtacacag gcacgtgcc actctgggtc atctatatcc gcaaccagca ccgctggacc 300  
 ctaggcctgc tggcctcgaa ggtgaccgcc tacatcttct tctgcaacat ctacgtcagc 360  
 atcctcttcc tgtgctgcat ctctgcgac cgcttcgtgg ccgtggtgta cgcgctggag 420  
 agtcggggcc gccgcgcgcg gaggaccgcc atcctcatct ccgcctgcat cttcatcctc 480  
 gtcgggatcg ttactaccc ggtgttccag acggaagaca aggagacctg ctttgacatg 540  
 ctgcagatgg acagcaggat tgccgggtac tactacgcca ggttcacctg tggctttgcc 600  
 atccctctct ccacatcgc cttcaccaac caccggattt tcaggagcat caagcagagc 660  
 atgggcttaa gcgctgcca gaaggccaag gtgaagcact cggccatcgc ggtggttgct 720  
 atcttcttag tctgcttcgc cccgtaccac ctggttctcc tcgtcaaagc cgctgccttt 780  
 tcctactaca gaggagacag gaacgccatg tgccgcttgg aggaaaggct gtacacagcc 840  
 tctgtggtgt ttctgtgcct gtccacggtg aacggcgctg ctgaccccat tatctacgtg 900  
 ctggccacgg accattccc ccaagaagtg tccagaatcc ataaggggtg gaaagagtgg 960  
 tccatgaaga cagacgtcac caggctcacc cacagcaggg acaccgagga gctgcagtgc 1020  
 cccgtggccc ttgcagacca ctacaccttc tccaggcccg tgcaccacc agggtcacca 1080  
 tgccctgcaa agaggctgat tgaggagtcc tgctga 1116

<210> 26  
 <211> 371  
 <212> PRT  
 <213> Homo sapiens

<400> 26

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser  
 1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser  
 20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
 35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln  
 50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
 65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
 85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile  
 100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
 115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
 130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
 145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
 165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
 180 185 190

Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
 195 200 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser  
 210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
 225 230 235 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
 245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
 260 265 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
 275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
 290 295 300

His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
 305 310 315 320



Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
 325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
 340 345 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
 355 360 365

Glu Ser Cys  
 370

<210> 27  
 <211> 1113  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 atggcgaact atagccatgc agctgacaac attttgcaaa atctctcgcc tctaacagcc 60  
 tttctgaaac tgacttcctt gggtttcata ataggagtca gcgtgggtggg caacctcctg 120  
 atctccattt tgctagtga agataagacc ttgcatagag caccttacta cttcctgttg 180  
 gatctttgct gttcagatat cctcagatct gcaatttggt tcccatttgt gttcaactct 240  
 gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgat tgcctttctg 300  
 ggggttttgt cctgtttcca cactgctttc atgctcttct gcatcagtgt caccagatac 360  
 ttagctatcg cccatcaccg cttctataca aagaggctga ccttttggac gtgtctggct 420  
 gtgatctgta tgggtgtggac tctgtctgtg gccatggcat ttccccggg tttagacgtg 480  
 ggcacttact cattcattag ggaggaagat caatgcacct tccaacaccg ctccttcagg 540  
 gctaattgatt ccttaggatt tatgctgctt cttgctctca tctccttagc cacacagctt 600  
 gtctacctca agctgatatt tttcgtccac gatcgaagaa aaatgaagcc agtccagttt 660  
 gtagcagcag tcagccagaa ctggactttt catggtcctg gagccagtgg ccaggcagct 720  
 gccaatggc tagcaggatt tggaaggggt cccacaccac ccaccttgct gggcatcagg 780  
 caaaatgcaa acaccacagg cagaagaagg ctattggtct tagacgagtt caaaatggag 840  
 aaaagaatca gcagaatgtt ctatataatg acttttctgt ttctaacctt gtggggcccc 900  
 tacctgggtg cctgttattg gagagttttt gcaagagggc ctgtagtacc agggggattt 960  
 ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatccttt tgtctgcatt 1020  
 ttctcaaaca gggagctgag gcgctgtttc agcacaacct ttctttactg cagaaaatcc 1080  
 aggttaccaa gggaacctta ctgtgttata tga 1113

<210> 28  
 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 28

Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser  
 1 5 10 15

Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly  
 20 25 30

Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp  
 35 40 45

Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys  
 50 55 60

Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser  
 65 70 75 80

Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val  
 85 90 95

Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu  
 100 105 110

Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe  
 115 120 125

Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met  
 130 135 140

Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val  
 145 150 155 160

Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His  
 165 170 175

Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala  
 180 185 190

Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe  
 195 200 205

Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val  
 210 215 220

Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala  
 225 230 235 240

Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu  
 245 250 255

Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu  
 260 265 270

Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr  
 275 280 285

Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala  
 290 295 300

Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe  
 305 310 315 320

Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro  
 325 330 335

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr  
 340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys  
 355 360 365

Val Ile  
 370

<210> 29

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 29

atgcagggtcc cgaacagcac cggcccggac aacgcgacgc tgcagatgct gcggaacccg 60

gogatcgcg tggccctgcc cgtggtgtac tcgctggtgg cggcggtcag catcccgggc 120

aacctcttct ctctgtgggt gctgtgccgg cgcattggggc ccagatcccc gtcggtcatc 180

ttcatgatca acctgagcgt cacggacctg atgctggcca gcgtgttgcc tttccaaatc 240

tactaccatt gcaaccgcca ccaactgggta ttccggggtgc tgctttgcaa cgtggtgacc 300

gtggcctttt acgcaaacat gtattccagc atcctcacca tgacctgtat cagcgtggag 360  
 cgcttcctgg gggctctgta cccgctcagc tccaagcgct ggcgcgcgcg tcgttacgcg 420  
 gtggccgcgt gtgcagggac ctggctgctg ctctgaccg ccctgtgccc gctggcgcgc 480  
 accgatctca cctacccggt gcacgccctg ggcatcatca cctgcttcga cgtcctcaag 540  
 tggacgatgc tcccagcgt ggccatgtgg gccgtgttcc tcttcaccat cttcatcctg 600  
 ctgttcctca tcccgttcgt gatcacctg gcttggtaca cggccacat cctcaagctg 660  
 ttgcgcacgg aggaggcgca cggccgggag cagcggaggc gcgcggtggg cctggcgcgc 720  
 gtggtcttgc tggcctttgt cacctgcttc gcccacaaca acttcgtgct cctggcgcac 780  
 atcgtgagcc gcctgttcta cggcaagagc tactaccacg tgtacaagct cagcgtgtgt 840  
 ctgagctgcc tcaacaactg tctggaccgc tttgtttatt actttgcgtc ccgggaattc 900  
 cagctgcgcc tgcgggaata tttgggctgc cgccgggtgc ccagagacac cctggacacg 960  
 cgccgcgaga gcctcttctc cgccaggacc acgtccgtgc gctccgaggc cgggtgcgcac 1020  
 cctgaagggg tggagggagc caccaggccc ggcctccaga ggcaggagag tgtgttctga 1080

<210> 30  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 30

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met  
 1 5 10 15

Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu  
 20 25 30

Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu  
 35 40 45

Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn  
 50 55 60

Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile  
 65 70 75 80

Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys  
 85 90 95

Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu

100

105

110

Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
 115 120 125

Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys  
 130 135 140

Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg  
 145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
 165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
 180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
 195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
 210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
 225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
 245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
 260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
 275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
 290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
 305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
 325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu

340

345

350

Gln Arg Gln Glu Ser Val Phe  
355

<210> 31  
<211> 1503  
<212> DNA  
<213> Homo sapiens

<400> 31  
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ccagtgcgag ccggggcgag ctccgggtgcc gcggcgagtg gcacaggctg gcagccatgg 120  
gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgcccg ccctttgcgt 180  
cgctggcccc cccctcgcg tgccagctcc agccccgccc ccggagcggc gtccgctcac 240  
tcggttcaag gcagcgcgac tgcgggtggc gcacgaccag ggcgcagacc ttggggcgcg 300  
cggcccatgg agtcggggct gctgcggcgg gcgcgggtga gcgaggtcat cgtcctgcat 360  
tacaactaca ccggcaagct ccgcggtgcg agctaccagc cgggtgccgg cctgcgcgcc 420  
gacgcgctgg tgtgcctggc ggtgtgcgcc ttcacgtgc tagagaatct agccgtgttg 480  
ttggtgctcg gacgccaccc gcgcttccac gctcccatgt tcctgctcct gggcagcctc 540  
acgttgctcg atctgctggc aggcgcggcc tacgcgcga acatcctact gtcggggccg 600  
ctcacgctga aactgtcccc cgcgctctgg ttgcacggg agggaggcgt ctctgtggca 660  
ctcactgcgt ccgtgctgag cctcctggcc atcgcgctgg agcgcagcct caccatggcg 720  
cgcagggggc ccgcgcccgt ctccagtcgg ggcgcacgc tggcgatggc agccgcggcc 780  
tggggcgtgt cgctgctcct cgggctcctg ccagcgtgg gctggaattg cctgggtcgc 840  
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cgggcgcgtc gcaagccgag ctctctggcc ttgctgcgca cgctcagcgt ggtgctcctg 1080  
gcctttgtgg catgttgggg cccctctctc ctgctgctgt tgctcgacgt ggcgtgccg 1140  
gcgcgcacct gtctgtact cctgcaggcc gatcccttcc tgggactggc catggccaac 1200  
tcacttctga acccatcat ctacacgctc accaaccgag acctgcgcca cgcgctcctg 1260  
cgctggtct gctgcggacg cactcctgc ggcagagacc cgagtggctc ccagcagtcg 1320  
gcgagcgcgg ctgaggcttc cgggggcctg cgcgctgcc tgccccggg ccttgatggg 1380  
agcttcagcg gtcggagcg ctcatcgccc cagcgcgacg ggctggacac cagcggctcc 1440

acaggcagcc ccggtgcacc cacagccgcc cggactctgg tatcagaacc ggctgcagac 1500  
tga 1503

<210> 32  
<211> 500  
<212> PRT  
<213> Homo sapiens  
<400> 32

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu  
1 5 10 15

Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala  
20 25 30

Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly  
35 40 45

Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala  
50 55 60

Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His  
65 70 75 80

Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg  
85 90 95

Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro  
100 105 110

Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg  
115 120 125

Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val  
130 135 140

Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu  
145 150 155 160

Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu  
165 170 175

Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala  
180 185 190

Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala  
 195 200 205

Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser  
 210 215 220

Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala  
 225 230 235 240

Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met  
 245 250 255

Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala  
 260 265 270

Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu  
 275 280 285

Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val  
 290 295 300

Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln  
 305 310 315 320

Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly  
 325 330 335

Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu  
 340 345 350

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro  
 355 360 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys  
 370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn  
 385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg  
 405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg  
 420 425 430



Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly  
 435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly  
 450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser  
 465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu  
 485 490 495

Pro Ala Ala Asp  
 500

<210> 33  
 <211> 1029  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
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 tacaaaatca cccaggtcct cttcccactg ctctacactg tcctgttttt tgttggactt 120  
 atcacaaatg gcctggcgat gaggattttc tttcaaattc ggagtaaata aaactttatt 180  
 atttttctta agaacacagt catttctgat cttctcatga ttctgacttt tccattcaaa 240  
 attcttagtg atgccaaact gggaacagga ccactgagaa cttttgtgtg tcaagttacc 300  
 tccgtcatat tttatttcac aatgtatatc agtatttcat tcctgggact gataactatc 360  
 gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctcttgggg 420  
 gctaagattc tctctgttgt catctgggca ttcatgttct tactctcttt gcctaacatg 480  
 attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctcttt ccttaaatca 540  
 gaggtcggtc tagtctggca tgaaatagta aattacatct gtcaagtcatt tttctggatt 600  
 aattttctta ttgttattgt atgttatata ctattacaa aagaactgta ccggtcatac 660  
 gtaagaacga ggggtgtagg taaagtcccc aggaaaaagg tgaacgtcaa agttttcatt 720  
 atcattgctg tattctttat ttgttttggt cctttccatt ttgccgaat tccttacacc 780  
 ctgagccaaa cccgggatgt ctttgactgc actgctgaaa atactctgtt ctatgtgaaa 840  
 gagagcactc tgtgggtaac ttccttaaat gcatgcctgg atccgttcat ctattttttc 900  
 ctttgcaagt cttcagaaa ttccttgata agtatgctga agtgcccaa ttctgcaaca 960  
 tctctgtccc aggacaatag gaaaaaagaa caggatgggtg gtgacccaaa tgaagagact 1020

ccaatgtaa

1029

<210> 34  
<211> 342  
<212> PRT  
<213> Homo sapiens

<400> 34

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu  
1 5 10 15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr  
20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg  
35 40 45

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys  
50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys  
65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val  
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile  
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg  
115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu  
130 135 140

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met  
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser  
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr  
180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys

195

200

205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg  
 210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile  
 225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg  
 245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala  
 260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser  
 275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser  
 290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr  
 305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro  
 325 330 335

Asn Glu Glu Thr Pro Met  
 340

&lt;210&gt; 35

&lt;211&gt; 1077

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

atgtcgggtct gctaccgtcc cccaggggaac gagacactgc tgagctggaa gacttcgcgg 60  
 gccacaggca cagccttctt gctgctggcg gcgctgctgg ggctgcctgg caacggcttc 120  
 gtggtgtgga gcttggcggg ctggcgccct gcacgggggc gaccgctggc ggccacgctt 180  
 gtgctgcacc tggcgctggc cgacggcgcg gtgctgctgc tcacgccgct ctttgtggcc 240  
 ttctgaccc ggcaggcctg gccgctgggc caggcgggct gcaaggcggg gtactacgtg 300  
 tgcgcgctca gcatgtacgc cagcgtgctg ctcaccggcc tgctcagcct gcagcgctgc 360  
 ctgcagtc cccgccctt cctggcgctt cggctgcgca gcccgccct ggcccgcgc 420  
 ctgctgctgg cggctctggc ggccgccctg ttgctcgccg tcccggccgc cgtctaccgc 480

cacctgtgga gggaccgcgt atgccagctg tgccaccgct cgcgcgtcca cgcgcgcgcc 540  
 cacctgagcc tggagactct gaccgctttc gtgcttccctt tcgggctgat gctcggctgc 600  
 tacagcgtga cgctggcacg gctgcggggc gcccgcctggg gctccggggc gcacggggcg 660  
 cgggtggggc ggctggtgag cgccatcgtg cttgccttcg gcttgctctg ggccccctac 720  
 cacgcagtca accttctgca ggcggtcgca gcgctggctc caccggaagg ggccttggcg 780  
 aagctggggc gagccggcca ggcggcgca gcgggaacta cggccttggc cttcttcagt 840  
 tctagcgtca acccggtgct ctacgtcttc accgctggag atctgctgcc ccgggcaggt 900  
 ccccgtttcc tcacgaggct cttcgaaggc tctggggagg cccgaggggg cggccgctct 960  
 agggaagggg ccatggagct ccgaactacc cctcagctga aagtgggtgg gcagggccgc 1020  
 ggcaatggag acccgggggg tgggatggag aaggacggtc cggaatggga cctttga 1077

<210> 36  
 <211> 358  
 <212> PRT  
 <213> Homo sapiens

<400> 36

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp  
 1 5 10 15

Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu  
 20 25 30

Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp  
 35 40 45

Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu  
 50 55 60

Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala  
 65 70 75 80

Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala  
 85 90 95

Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr  
 100 105 110

Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu  
 115 120 125

Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala  
 130 135 140

Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg  
 145 150 155 160

His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val  
 165 170 175

His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu  
 180 185 190

Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu  
 195 200 205

Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg  
 210 215 220

Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr  
 225 230 235 240

His Ala Val Asn Leu Leu Gln Ala Val Ala Ala Leu Ala Pro Pro Glu  
 245 250 255

Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly  
 260 265 270

Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr  
 275 280 285

Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu  
 290 295 300

Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser  
 305 310 315 320

Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val  
 325 330 335

Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp  
 340 345 350

Gly Pro Glu Trp Asp Leu  
 355

<210> 37  
 <211> 1005  
 <212> DNA  
 <213> Homo sapiens

<400> 37  
 atgctgggga tcatggcatg gaatgcaact tgcaaaaact ggctggcagc agaggctgcc 60  
 ctggaaaagt actacctttc ctttttttat gggattgagt tcgttggtggg agtccttgga 120  
 aataccattg ttgtttacgg ctacatcttc tctctgaaga actggaacag cagtaatatt 180  
 tatctcttta acctctctgt ctctgactta gcttttctgt gcacctccc catgctgata 240  
 aggagttatg ccaatggaaa ctggatatat ggagacgtgc tctgcataag caaccgatat 300  
 gtgcttcatg ccaacctcta taccagcatt ctctttctca cttttatcag catagatcga 360  
 tacttgataa ttaagtatcc tttccgagaa caccttctgc aaaagaaaga gtttgctatt 420  
 ttaatctcct tggccatttg ggttttagta accttagagt tactacccat acttcccctt 480  
 ataaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac 540  
 cccaactaca acctcattta cagcatgtgt ctaacactgt tgggggttcct tattcctctt 600  
 tttgtgatgt gtttctttta ttacaagatt gctctcttcc taaagcagag gaataggcag 660  
 gttgctactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720  
 ttctctgtgc tttttacacc ctatcacgtc atgoggaatg tgaggatcgc ttcacgcctg 780  
 gggagttgga agcagtatca gtgcactcag gtcgtcatca actcctttta cattgtgaca 840  
 cggccttttg cctttctgaa cagtgtcatc aacctgtct tctattttct tttgggagat 900  
 cacttcaggg acatgctgat gaatcaactg agacacaact tcaaaccct tacatccttt 960  
 agcagatggg ctcatgaact cctactttca ttcagagaaa agtga 1005

<210> 38  
 <211> 334  
 <212> PRT  
 <213> Homo sapiens

<400> 38

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala  
 1 5 10 15

Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile  
 20 25 30

Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr  
 35 40 45

Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn  
 50 55 60 /  
 Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile  
 65 70 75 80  
 Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile  
 85 90 95  
 Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe  
 100 105 110  
 Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe  
 115 120 125  
 Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu  
 130 135 140  
 Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu  
 145 150 155 160  
 Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala  
 165 170 175  
 Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr  
 180 185 190  
 Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr  
 195 200 205  
 Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala  
 210 215 220  
 Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile  
 225 230 235 240  
 Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile  
 245 250 255  
 Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val  
 260 265 270  
 Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser  
 275 280 285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp  
 290 295 300

Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe  
 305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys  
 325 330

<210> 39  
 <211> 1296  
 <212> DNA  
 <213> Homo sapiens

<400> 39

atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg	60
acgcggggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg	120
ccgggaacgcg ccaagctggc cctcgtgctc accggcgctgc tcattcttcgc cctggcgctc	180
tttggcaatg ctctggtgtt ctacgtggtg accgcgagca aggccatgcg caccgtcacc	240
aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc	300
gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg	360
gtgccatttg tccagtctac cgctgtttgt acagaaatgc tcactatgac ctgcattgct	420
gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga	480
agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg	540
tggcacgtgc aacaacttga gatcaaata gacttcctat atgaaaagga acacatctgc	600
tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgtc	660
atcctcttcc tctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa	720
ctttggataa agaaaagagt tggggatggt tcagtgcctc gaactattca tggaaaagaa	780
atgtccaaaa tagccaggaa gaagaaacga gctgtcatta tgatggtgac agtgggtggct	840
ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat	900
tttgaaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt	960
ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa	1020
aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacia	1080
aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagttttc cctcagagag	1140
aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg	1200
tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa	1260



ctggctgaga attctccttt agacagtggg catta

1296

<210> 40  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 40

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg  
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu  
100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro

195

200

205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
 210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
 225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
 245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val  
 260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
 275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
 290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
 305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
 325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
 340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
 355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
 370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
 385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
 405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
 420 425 430

&lt;210&gt; 41

<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 41	
ctgtgtacag cagttcgag agtg	24
<210> 42	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 42	
gagtgccagg cagagcaggt agac	24
<210> 43	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 43	
cccgaattcc tgcttgctcc cagcttgcc c	31
<210> 44	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 44	
tgtggatcct gctgtcaaag gtcccattcc gg	32
<210> 45	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 45	
tcacaatgct aggtgtgggc	20
<210> 46	

<211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 46  
 tgcataagaca atgggattac ag

22

<210> 47  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 tcacaatgct aggtgtgggc tggctgggtg cagtcacgt aggatcacc atgtggcacg 60  
 tgcaacaact tgagatcaaa tatgacttcc tatatgaaaa ggaacacatc tgctgcttag 120  
 aagagtggac cagccctgtg caccagaaga tctacaccac ctccatcctt gtcacccctc 180  
 tcctcctgcc tcttatgggtg atgcttattc tgtacgtaaa attgggttatg aactttggat 240  
 aaagaaaaga gttgggggatg gttcagtgc tgcgaactatt catggaaaag aaatgtccaa 300  
 aatagccagg aagaagaaac gagctgtcat tatgatgggtg acagtgggtg ctctctttgc 360  
 tgtgtgctgg gcaccattcc atgttgcca tatgatgatt gaatacagta attttgaaaa 420  
 ggaatatgat gatgtcaca tcaagatgat ttttgctatc gtgcaaatta ttggattttc 480  
 caactccatc tgtaatccca ttgtctatgc a 511

<210> 48  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 48  
 ctgcttagaa gagtggacca g

21

<210> 49  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 49  
 ctgtgcacca gaagatctac ac

22

<210> 50	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 50	
caaggatgaa ggtggtgtag a	21
<210> 51	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 51	
gtgtagatct tctggtgcac agg	23
<210> 52	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 52	
gcaatgcagg tcatagtgag c	21
<210> 53	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 53	
tggagcatgg tgacgggaat gcagaag	27
<210> 54	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 54	
gtgatgagca ggctactgag cgccaag	27

<210> 55  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 55  
gcaatgcagg cgcttaacat tac

23

<210> 56  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 56  
ttgggttaca atctgaaggg ca

22

<210> 57  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 57  
actccgtgtc cagcaggact ctg

23

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 58  
tgcgtgttcc tggaccctca cgtg

24

<210> 59  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 59  
caggccttgg attttaatgt cagggatgg

29

<210> 60	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 60	
ggagagtcag ctctgaaaga attcagg	27
<210> 61	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 61	
tgatgtgatg ccagatacta atagcac	27
<210> 62	
<211> 27	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 62	
cctgattcat ttaggtgaga ttgagac	27
<210> 63	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 63	
cccaagcttc ccaggtgta tttgat	26
<210> 64	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Novel Sequence	
<400> 64	
gttggatcca cataatgcat tttctc	26

<210> 65  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 atgattctca actcttctac tgaagatggg attaaaagaa tccaagatga ttgtcccaaa 60  
 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaaacag cttgggtggg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcaactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtatth ttcatgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaat 600  
 atactgggtt tcctgtttcc ttttctgac attcttacia gttatactct tatttgaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720  
 ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact 780  
 tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840  
 gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900  
 ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960  
 cccccaaaag ccaaatccca ctcaaaccct tcaacaaaaa tgagcacgct ttcctaccgc 1020  
 ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga gggttgagtga 1080

<210> 66  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 66

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45



Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
 145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
 195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
 245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
 260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
 325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
 340 345 350

Ala Pro Cys Phe Glu Val Glu  
 355

<210> 67  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 67  
 accatgggca gcccctggaa cggcagc

27

<210> 68  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 68  
 agaaccacca ccagcaggac gcggacggtc tgccggtgg

39

<210> 69  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 69  
 gtccgcgtcc tgctggtggt ggttctggca ttataatt

39

<210> 70  
 <211> 33

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Novel Sequence  
  
 <400> 70  
 cctggatcct tatcccatcg ttttcacgtt agc 33

<210> 71  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Novel Sequence  
  
 <400> 71  
 ctggaattct cctgccagca tggatga 26

<210> 72  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Novel Sequence  
  
 <400> 72  
 gcaggatcct atattgcgtg ctctgtcccc 30

<210> 73  
 <211> 999  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 73  
 atggtgaact ccaccaccg tgggatgcac acttctctgc acctctggaa ccgcagcagt 60  
 tacagactgc acagcaatgc cagtgagtc cttggaaaag gctactctga tggaggggtgc 120  
 tacgagcaac tttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagcttggtg 180  
 gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240  
 tttttcatct gcagcttggc tgtggctgat atgctgggtga gcgtttcaaa tggatcagaa 300  
 accattatca tcaccctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360  
 attgataatg tcattgactc ggtgatctgt agctccttgc ttgcatccat ttgcagcctg 420  
 ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480  
 atgacagtta agcgggttgg gatcagcata agttgtatct gggcagcttg cacggtttca 540  
 ggcattttgt tcatcattta ctcagatagt agtgctgtca tcatctgcct catcaccatg 600

ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttcct gatggccagg 660  
 cttcacatta agaggattgc tgtcctcccc ggcactgggtg ccatccgcca aggtgccaat 720  
 atgaagggag cgattacctt gaccatcctg attggcgtct ttgttgctctg ctgggccccca 780  
 ttcttcctcc acttaatatt ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840  
 atgtctcact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900  
 atttatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960  
 cccctgggag gcctttgtga cttgtctagc agatattaa 999

<210> 74  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 74

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp  
 1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly  
 20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro  
 35 40 45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu  
 50 55 60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
 65 70 75 80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
 85 90 95

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr  
 100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
 115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
 130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
 145 150 155 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys  
210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
225 230 235 240

Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
325 330

<210> 75

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 75

ccgaagcttc gagctgagta aggcggcggg ct

32

<210> 76

<211> 31

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 76  
gtggaattca tttgccctgc ctcaaccccc a

31

<210> 77  
<211> 1344  
<212> DNA  
<213> Homo sapiens

<400> 77  
atggagctgc taaagctgaa ccggagcgtg cagggaaccg gaccggggcc gggggcttcc 60  
ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120  
ccccctcgca ttgcgggagc cgggacacga gaattggagc tggccattag aatcactctt 180  
tacgcagtga tcttctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240  
ctgagccgcc gcctgaggac tgtcaccaat gccttctcc tctcactggc agtcagcgac 300  
ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360  
atctttggca ccgtcatctg caaggcgggt tctacctca tgggggtgtc tgtgagtgtg 420  
tccacgctaa gcctcgtggc catcgcaact gagcgatata gcgccatctg ccgaccactg 480  
caggcacgag tgtggcagac gcgctccac gcggctcgcg tgattgtagc cacgtggctg 540  
ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600  
cgtgtgctgc agtgctgca tcgctggccc agtgcgcggg tccgccagac ctggtccgta 660  
ctgctgcttc tgetcttgtt ctcatccca ggtgtgggta tggccgtggc ctacgggctt 720  
atctctcgcg agctctactt agggcttcgc tttagcggcg acagtgcagc cgacagccaa 780  
agcagggtcc gaaaccaagg cgggctgcc a ggggtgttc accagaacgg gcgttgccgg 840  
cctgagactg gcgcggttg caaagacagc gatggctgct acgtgcaact tccacgttcc 900  
cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960  
accaggcca agctgctggc taagaagcgc gtgggtgcga tgttgctggg gatcgttgtg 1020  
cttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcgc ctttgatggc 1080  
ccgggtgcac accgagcact ctccgggtgct cctatctcct tcattcactt gctgagctac 1140  
gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgtt tcgccaggcc 1200  
tgcttgaaa cttgcgctcg ctgctgccc cggcctccac gagctcggcc cagggtcttt 1260  
ccgatgagg accctccac tccctccatt gcttcgtgt ccaggcttag ctacaccacc 1320

atcagcacac tgggccctgg ctga

1344

<210> 78  
<211> 447  
<212> PRT  
<213> Homo sapiens

<400> 78

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
1 5 10 15

Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
 210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
 225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
 245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
 260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
 275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
 290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
 305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu  
 325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
 340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
 355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
 370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
 385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
 405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
 420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly  
 435 440 445



<210> 79  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 79  
 tgcaagctta aaaaggaaaa aatgaacagc

30

<210> 80  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 80  
 taaggatccc ttcccttcaa aacatccttg

30

<210> 81  
 <211> 1014  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
 atgaacagca catgtattga agaacagcat gacctggatc actatttgtt tcccattgtt 60  
 tacatctttg tgattatagt cagcattcca gccaatattg gatctctgtg tgtgtctttc 120  
 ctgcaaccca agaaggaaag tgaactagga atttacctct tcagtttgtc actatcagat 180  
 ttactctatg cattaactct ccctttatgg attgattata cttggaataa agacaactgg 240  
 actttctctc ctgccttgtg caaagggagt gcttttctca tgtacatgaa gttttacagc 300  
 agcacagcat tcttcacctg cattgccgtt gatcgggtatt tggctgttgt ctaccctttg 360  
 aagttttttt tcttaaggac aagaagaatt gcactcatgg tcagcctgtc catctggata 420  
 ttggaaacca tcttcaatgc tgtcatgttg tgggaagatg aaacagttgt tgaatattgc 480  
 gatgocgaaa agtctaattt tactttatgc tatgacaaat accctttaga gaaatggcaa 540  
 atcaacctca acttgttcag gacgtgtaca ggctatgcaa tacctttggg caccatcctg 600  
 atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa 660  
 aagaagagaa tcataaaaact acttgtcagc atcacagtta cttttgtctt atgctttact 720  
 ccctttcatg tgatgttgct gattcgctgc attttagagc atgctgtgaa cttcgaagac 780  
 cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacggttgc attaacaagt 840

ttaaattgtg ttgctgatcc aattctgtac tgttttgta ccgaaacagg aagatatgat 900  
 atgtggaata tattaataatt ctgcactggg aggtgtaata catcaciaag acaaagaaaa 960  
 cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag 1014

<210> 82  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 82

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu  
 1 5 10 15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn  
 20 25 30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu  
 35 40 45

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala  
 50 55 60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp  
 65 70 75 80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met  
 85 90 95

Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg  
 100 105 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg  
 115 120 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile  
 130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys  
 145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu  
 165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr  
 180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln  
195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile  
210 215 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
325 330 335

Glu

<210> 83  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 83  
caggaagaag aaacgagctg tcattatgat ggtgacagtg

40

<210> 84  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Novel Sequence  
 <400> 84  
 cactgtcacc atcataatga cagctcgttt cttcttctg 40  
 <210> 85  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Novel Sequence  
 <400> 85  
 ggccaccggc agaccaaacg cgtcctgctg 30  
 <210> 86  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Novel Sequence  
 <400> 86  
 ctcttcggg cctcctatcg ttgtcagaag t 31  
 <210> 87  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Novel Sequence  
 <400> 87  
 ggaaaagaag agaatcaaaa aactacttgt cagcatc 37  
 <210> 88  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Novel Sequence  
 <400> 88  
 ctcttcggg cctcctatcg ttgtcagaag t 31  
 <210> 89  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens  
 <400> 89

atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60  
 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtecca aaattcaacc cttccgatag ggctgggcct gacaaaaaat 600  
 atactgggtt tctgttttcc ttttctgac attcttaciaa gttatactct tatttggaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tattaataag 720  
 ataattatgg caattgtgct tttcttttcc ttttctgga ttccccacca aatattcact 780  
 tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840  
 gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900  
 ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960  
 cccccaaaag ccaaattcca ctcaaaccct tcaacaaaaa tgagcacgct ttcctaccgc 1020  
 ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga gggtgagtga 1080

<210> 90  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 90

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
 145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
 195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys  
 225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
 245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
 260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
 325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
 340 345 350

Ala Pro Cys Phe Glu Val Glu  
 355

<210> 91  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 91  
 ccaagaaatg atgatattaa aaagataatt atggc

35

<210> 92  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 92  
 ctcttcggt cctcctatcg ttgtcagaag t

31

<210> 93  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
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 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt ttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300  
 tgtgaagattg cttcagccag cgtcagtttc gccctgtaog ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420

acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtatatt ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaaat 600  
 atactgggtt tctgtttcc ttttctgac attcttaca gttatactct tatttggaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720  
 ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact 780  
 tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840  
 gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900  
 ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960  
 cccccaaaag ccaaatccca ctcaaaccct tcaacaaaaa tgagcacgct ttctaccgc 1020  
 ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga gggttgagtga 1080

<210> 94  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 94

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125



Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
 145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
 195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
 245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
 260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
 275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
 290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
 305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
 325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
 340 345 350

Ala Pro Cys Phe Glu Val Glu  
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gtgggaatat ttggaacag cttggtggtg atagtcattt acttttatat gaagctgaag	180
actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact	240
ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta	300
tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg	360
tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ctttcgacgc	420
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gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaat	600
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cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca agttaagaag	720
ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact	780
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gacacggcca tgcctatcac catttgata gcttatttta acaattgcct gaatcctctt	900
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ccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttctaccgc	1020
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<400> 100

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			20					25					30		

Thr	Leu	Tyr	Ser	Ile	Ile	Phe	Val	Val	Gly	Ile	Phe	Gly	Asn	Ser	Leu
		35					40					45			

Val	Val	Ile	Val	Ile	Tyr	Phe	Tyr	Met	Lys	Leu	Lys	Thr	Val	Ala	Ser
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Val	Phe	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Cys	Phe	Leu	Leu	Thr
65					70					75					80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
                     85                    90                    95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
                     100                    105                    110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
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Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
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Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
                     145                    150                    155                    160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
                     165                    170                    175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
                     180                    185                    190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
                     195                    200                    205

Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys  
                     210                    215                    220

Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys  
                     225                    230                    235                    240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
                     245                    250                    255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
                     260                    265                    270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
                     275                    280                    285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
                     290                    295                    300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
                     305                    310                    315                    320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
 325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
 340 345 350

Ala Pro Cys Phe Glu Val Glu  
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37

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<400> 102  
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33

<210> 103  
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 <212> DNA  
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<400> 103  
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62

<210> 104  
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62

<210> 105  
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<212> DNA  
<213> Homo sapiens

<400> 105

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gtgggaatat ttggaaacag cttggtggtg atagtcatTT acttttatat gaagctgaag    180
actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact    240
ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta    300
tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtggt tctactcacg    360
tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc    420
acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt    480
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atactgggtt tcctgtttcc ttttctgac attccttaca gttatactct tatttggaag    660
gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag    720
ataattatgg cagcaattgt gcttttcttt ttcttttctt ggattcccca ccaaattatc    780
acttttctgg atgtattgat tcaactaggc atcatagctg actgtagaat tgcagatatt    840
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 20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
 85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
 100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
 115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
 130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
 145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
 165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
 180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
 195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
 210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
 225 230 235 240

Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Ser Trp Ile Pro  
 245 250 255

His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile  
 260 265 270

Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr  
 275 280 285

Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly  
 290 295 300

Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr  
 305 310 315 320

Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser  
 325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys  
 340 345 350

Pro Ala Pro Cys Phe Glu Val Glu  
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26

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 <212> DNA  
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38

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<400> 109  
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<400> 110  
gttgatcca cataatgcat tttctc 26

<210> 111  
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<400> 112

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Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
 20 25 30

Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
 35 40 45

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
 50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
 65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
 85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
 100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
 115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
 130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
 145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
 165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
 180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
 195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
 210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
 225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
 245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
 260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
 275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
 290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
 305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu  
 325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
 340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
 355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
 370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
 385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
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<210> 117  
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aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200  
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<210> 128  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 128

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg  
1 5 10 15

Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg  
20 25 30

Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu  
 35 40 45

Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala  
 50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr  
 65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe  
 85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu  
 100 105 110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
 115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
 130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
 145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
 165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
 180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
 195 200 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
 210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
 225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
 245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Lys  
 260 265 270



Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
 275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
 290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
 305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
 325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
 340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
 355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
 370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
 385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
 405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
 420 425 430

<210> 129

<211> 2040

<212> DNA

<213> Homo sapiens

<400> 129

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gtgaccgctg tgtgcctgtg cctgttcgtc gtcgggggtga gcggcaacgt ggtgaccgtg	180
atgctgatcg ggcgctaccg ggacatgcgg accaccacca acttgtaacct gggcagcatg	240
gccgtgtccg acctactcat cctgctcggg ctgcogttcg acctgtaccg cctctgggcg	300
tcgcggccct ggggtgttcgg gccgctgctc tgccgcctgt ccctctacgt gggcgagggc	360

tgcacctacg ccacgctgct gcacatgacc gcgctcagcg tcgagcgcta cctggccatc	420
tgccgccccg tccgcgcccc cgtcttggtc acccggcgcc gcgtccgcgc gctcatcgct	480
gtgctctggg ccgtggcgct gctctctgcc ggtcccttct tgttcctggt gggcgctgag	540
caggaccccc gcctctccgt agtccccggc ctcaatggca ccgcgcggat cgcctcctcg	600
cctctcgctt cgtcgccgcc tctctggctc tcgcggggcg caccgcgctc cccgccgctc	660
gggcccagaga ccgcggaggc cgcggcgctg ttcagccgcg aatgccggcc gagccccgcg	720
cagctggggc cgctgctgtg catgctgtgg gtcaccaccg cctacttctt cctgcccttt	780
ctgtgcctca gcctcctcta cgggctcatc gggcgggagc tgtggagcag ccggcgggcg	840
ctgcgaggcc cggccgcctc gggcggggag agaggccacc ggcagaccaa acgcgtcctg	900
cgtaagtgga gccgccgtgg ttccaaagac gcctgcctgc agtcgcgccc gccggggacc	960
gcgcaaacgc tgggtccctt tcccctgctc gccagctctt gggcgccgct tccagctccc	1020
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tcctgtcccc caggagctct gggggacccc agggcgcttt gaggggtggga tccccggatc	1140
cgattcagta accagcagtg cttttccaga gcctctgaga ccagaaagga gagttggtaa	1200
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agacgagggg gatttcatta agctaaaatt ttttatttaa tgttaagtga tgctgaaggc	1320
taaagtaaac cttgctcgta tcaaaaagta aagattgtgc agacctgttg tagaattctt	1380
ttcaacagag aacagaaaac ttgtctccga agtggggttg tggaaggaag cctgccaaag	1440
cggcttggtc agagaaattg ctcttctggt tttatgtcca gccttgataa cacatatggg	1500
agcctactat gcagttttta agcaagtatc catgcagcct gcagcctggt cattttttct	1560
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aagtccaggc cgagaggctt ccacagaagc agggacactg cgggggaagt tgcaggggac	1980
actggaggag acacggtggg ctacaccgag acaagcgcta acgtgaagac gatgggataa	2040

<210> 130  
 <211> 412  
 <212> PRT

<213> Homo sapiens

<400> 130

Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu  
1 5 10 15

Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro  
20 25 30

Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu  
35 40 45

Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly  
50 55 60

Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met  
65 70 75 80

Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr  
85 90 95

Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg  
100 105 110

Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His  
115 120 125

Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu  
130 135 140

Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala  
145 150 155 160

Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu  
165 170 175

Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn  
180 185 190

Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu  
195 200 205

Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr  
210 215 220

Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala  
 225 230 235 240

Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe  
 245 250 255

Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg  
 260 265 270

Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly  
 275 280 285

Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val  
 290 295 300

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile  
 305 310 315 320

Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe  
 325 330 335

Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro  
 340 345 350

Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys  
 355 360 365

Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg  
 370 375 380

Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly  
 385 390 395 400

Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly  
 405 410

<210> 131

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 131

atggagctgc taaagctgaa ccggagcgtg cagggaaccg gaccggggcc gggggcttcc 60

ctgtgccgcc cgggggccc tctctcaac agcagcagtg tgggcaacct cagctgcgag 120

ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180

taacgagtga tcttcctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga	240
ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcactggc agtcagcgac	300
ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc	360
atctttggca cgcgcactctg caaggcgggtt tcctacctca tgggggtgtc tgtgagtgtg	420
tccacgctaa gcctcgtggc catcgcaactg gagcgatata gcgccatctg ccgaccactg	480
caggcacgag tgtggcagac gcgctccac gcggctcgcg tgattgtagc cacgtggctg	540
ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct	600
cgtgtgctgc agtgcggtgca tcgctggccc agtgcgcggg tccgccagac ctgggtccgta	660
ctgctgcttc tgctcttggt cttcatccca ggtgtggtta tggccgtggc ctacgggctt	720
atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgacag cgacagccaa	780
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cctgagactg gcgcggttg caaagacagc gatggctgct acgtgcaact tccacgttcc	900
cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc	960
accagggcca agctgctggc taagaagcgc gtgaaacgaa tgttgctggt gatcgttgtg	1020
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cgggtgac accgagcact ctcggtgct cctatctcct tcattcactt gctgagctac	1140
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tgcttgaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggtcttt	1260
cccgatgagg accctccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc	1320
atcagcacac tgggccctgg ctga	1344

<210> 132  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 132

Met	Glu	Leu	Leu	Lys	Leu	Asn	Arg	Ser	Val	Gln	Gly	Thr	Gly	Pro	Gly
1				5					10					15	

Pro	Gly	Ala	Ser	Leu	Cys	Arg	Pro	Gly	Ala	Pro	Leu	Leu	Asn	Ser	Ser
			20					25					30		

Ser	Val	Gly	Asn	Leu	Ser	Cys	Glu	Pro	Pro	Arg	Ile	Arg	Gly	Ala	Gly
		35					40					45			

Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
 50 55 60

Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
 65 70 75 80

Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
 85 90 95

Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
 100 105 110

Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
 115 120 125

Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
 130 135 140

Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
 145 150 155 160

Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
 165 170 175

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
 180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
 195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
 210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
 225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
 245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
 260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
 275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
 290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
 305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu  
 325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
 340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
 355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
 370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
 385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
 405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
 420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly  
 435 440 445

<210> 133

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 133

atgaacagca catgtattga agaacagcat gacctggatc actatttggt tccattggt 60

tacatctttg tgattatagt cagcattcca gccaatattg gatctctgtg tgtgtctttc 120

ctgcaagcaa agaaggaaag tgaactagga atttacctct tcagtttggtc actatcagat 180

ttactctatg cattaactct ccctttatgg attgattata cttggaataa agacaactgg 240

actttctctc ctgccttggt caaaggagg gcttttctca tgtacatgaa tttttacagc 300

agcacagcat tcctcacctg cattgccgtt gatcggtatt tggctgttgt ctaccctttg 360

aagttttttt tcctaaggac aagaagattt gcactcatgg tcagcctgtc catctggata 420

ttggaaacca tcttcaatgc tgtcatgttg tgggaagatg aaacagttgt tgaatattgc	480
gatgccgaaa agtctaattt tactttatgc tatgacaaat accctttaga gaaatggcaa	540
atcaacctca acttgttcag gacgtgtaca ggctatgcaa tacctttggt caccatcctg	600
atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa	660
aagaagagaa tcaaaaaact acttgtcagc atcacagtta cttttgtctt atgctttact	720
ccctttcatg tgatgttgct gattcgctgc attttagagc atgctgtgaa cttcgaagac	780
cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacgggttg attaacaagt	840
ttaaattgtg ttgctgatcc aattctgtac tgttttgtta ccgaaacagg aagatatgat	900
atgtggaata tattaaaatt ctgcactggg aggtgtaata catcacaaag acaaagaaaa	960
cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag	1014

<210> 134  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 134

Met	Asn	Ser	Thr	Cys	Ile	Glu	Glu	Gln	His	Asp	Leu	Asp	His	Tyr	Leu
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Phe	Pro	Ile	Val	Tyr	Ile	Phe	Val	Ile	Ile	Val	Ser	Ile	Pro	Ala	Asn
		20						25					30		

Ile	Gly	Ser	Leu	Cys	Val	Ser	Phe	Leu	Gln	Ala	Lys	Lys	Glu	Ser	Glu
	35						40					45			

Leu	Gly	Ile	Tyr	Leu	Phe	Ser	Leu	Ser	Leu	Ser	Asp	Leu	Leu	Tyr	Ala
50						55					60				

Leu	Thr	Leu	Pro	Leu	Trp	Ile	Asp	Tyr	Thr	Trp	Asn	Lys	Asp	Asn	Trp
65					70					75					80

Thr	Phe	Ser	Pro	Ala	Leu	Cys	Lys	Gly	Ser	Ala	Phe	Leu	Met	Tyr	Met
			85						90					95	

Asn	Phe	Tyr	Ser	Ser	Thr	Ala	Phe	Leu	Thr	Cys	Ile	Ala	Val	Asp	Arg
			100					105					110		

Tyr	Leu	Ala	Val	Val	Tyr	Pro	Leu	Lys	Phe	Phe	Phe	Leu	Arg	Thr	Arg
	115						120					125			



Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile  
 130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys  
 145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu  
 165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr  
 180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln  
 195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile  
 210 215 220

Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
 225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
 245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
 260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
 275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
 290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
 305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
 325 330 335

Glu

<210> 135  
 <211> 999  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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tacagactgc acagcaatgc cagtgagtc cttggaaaag gctactctga tggaggggtgc 120  
tacgagcaac tttttgtctc tcctgaggtg tttgtgactc tgggtgtcat cagcttggtg 180  
gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240  
tttttcatct gcagcttggc tgtggctgat atgctgggtga gcgtttcaaa tggatcagaa 300  
accattatca tcacctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360  
attgataatg tcattgactc ggtgatctgt agctccttgc ttgcatccat ttgcagcctg 420  
ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480  
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ggcattttgt tcatcattta ctcatagat agtgctgtca tcatctgcct catcaccatg 600  
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cttcacatta agaggattgc tgtcctcccc ggcactgggtg ccatccgcca aggtgccaat 720  
atgaaggga aaattacctt gaccatcctg attggcgtct ttgttgtctg ctgggccccca 780  
ttcttctctc acttaatat ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840  
atgtctcact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900  
atztatgcac tccggagtca agaactgagg aaaacottca aagagatcat ctgttgctat 960  
cccctgggag gcctttgtga cttgtctagc agatattaa 999

<210> 136  
<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 136

Met	Val	Asn	Ser	Thr	His	Arg	Gly	Met	His	Thr	Ser	Leu	His	Leu	Trp
1				5				10					15		
Asn	Arg	Ser	Ser	Tyr	Arg	Leu	His	Ser	Asn	Ala	Ser	Glu	Ser	Leu	Gly
			20					25					30		
Lys	Gly	Tyr	Ser	Asp	Gly	Gly	Cys	Tyr	Glu	Gln	Leu	Phe	Val	Ser	Pro
	35						40					45			
Glu	Val	Phe	Val	Thr	Leu	Gly	Val	Ile	Ser	Leu	Leu	Glu	Asn	Ile	Leu
	50					55					60				

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
65 70 75 80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
85 90 95

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr  
100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
145 150 155 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys  
210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
225 230 235 240

Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
 305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
 325 330

<210> 137  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 137  
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<210> 138  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Novel Sequence

<400> 138  
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<210> 139  
 <211> 1842  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 gtagacctaa tcggcaactc catgggtcatt ttggctgtga cgaagaacaa gaagctccgg 180  
 aattctggca acatcttcgt ggtcagtcct tctgtggccg atatgctggg ggccatctac 240  
 ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300  
 tgccagatgg tcgggttcat cacagggtcg agtgtggtcg gctccatctt caacatcgtg 360  
 gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagtacga acggatcttc 420  
 agtgtgcgca atacctgcat ctacctgggc atcacctgga tcatgaccgt cctggctgtc 480  
 ctgcccacaa tgtacattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc 540  
 aactatctga acaaccctgt cttcactgtt accatcgtct gcatccactt cgtcctccct 600  
 ctctcatcg tgggtttctg ctacgtgagg atctggacca aagtgtctgg ggcctgtgac 660

cctgcagggc agaatcctga caaccaactt gctgaggttc gcaattttct aaccatgttt 720  
gtgatcttcc tctcttttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780  
gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840  
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catgctcgcg accaagctcg tgaacaagac cgtgcccattg cctgtcctgc tgtggaggaa 1080  
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tctaccacc acaagtctgt ctttagccac tccaaggctg cctctggtca cctcaagcct 1260  
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cccatcaagc cagctaccag ccatgctgag ccaccactg ctgactatcc caagcctgcc 1560  
actaccagcc accctaagcc cgctgctgct gacaaccctg agctctctgc ctcccattgc 1620  
cccagatcc ctgccattgc ccaccctgtg totgacgaca gtgacctccc tgagtcggcc 1680  
tctagccctg ccgctgggcc caccaagcct gctgccagcc agctggagtc tgacaccatc 1740  
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gttggtgatg ttgaagatga tctgatgaa atggctgtgt ga 1842

<210> 140  
<211> 613  
<212> PRT  
<213> Homo sapiens

<400> 140

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys  
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Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe  
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Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met  
35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn  
 50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr  
 65 70 75 80

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu  
 85 90 95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val  
 100 105 110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys  
 115 120 125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn  
 130 135 140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
 145 150 155 160

Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr  
 165 170 175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
 180 185 190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr  
 195 200 205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln  
 210 215 220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe  
 225 230 235 240

Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu  
 245 250 255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro  
 260 265 270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys  
 275 280 285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu  
 290 295 300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro  
 305 310 315 320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala  
 325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala  
 340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
 355 360 365

Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
 370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala  
 385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
 405 410 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
 420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly  
 435 440 445

Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
 450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
 465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr  
 485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
 500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
 515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro  
 530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
 545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu  
 565 570 575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser  
 580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Asp Val Glu Asp Asp Pro  
 595 600 605

Asp Glu Met Ala Val  
 610

<210> 141  
 <211> 1842  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 gtagacctaa tcggcaactc catgggtcatt ttggctgtga cgaagaacaa gaagctccgg 180  
 aattctggca acatcttcgt ggtcagtctc tctgtggccg atatgctggg ggccatctac 240  
 ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300  
 tgccagatgg tcgggttcat cacagggtcg agtgtggctg gctccatctt caacatcggt 360  
 gcaatcgcta tcaaccgtta ctgtacata tgccacagcc tccagtacga acggatcttc 420  
 agtgtgcgca atacctgcat ctacctgggc atcacctgga tcatgaccgt cctggctgtc 480  
 ctgccaaca tgtagattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc 540  
 aactatctga acaaccctgt cttcactgtt accatcgctc gcatccaact cgtcctccct 600  
 ctctcatcg tgggtttctg ctacgtgagg atctggacca aagtgtggc ggcccgtgac 660  
 cctgcagggc agaactctga caaccaactt gctgaggttc gcaataaact aaccatgttt 720  
 gtgatcttcc tctcttttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780  
 gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840  
 ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat 900



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 ggccctcatca gtgatattcg tgagatgcag gaggcccgta ccctggcccg cgcccgtgcc 1020  
 catgctcgcg accaagctcg tgaacaagac cgtgcccatg cctgtcctgc tgtggaggaa 1080  
 accccgatga atgtccggaa tgttccatta cctggtgatg ctgcagctgg ccaccccgac 1140  
 cgtgcctctg gccaccctaa gcccattcc agatcctcct ctgcctatcg caaatctgcc 1200  
 tctaccacc acaagtctgt ctttagccac tccaaggctg cctctggtca cctcaagcct 1260  
 gtctctggcc actccaagcc tgctctggtt caccccaagt ctgccactgt ctaccctaag 1320  
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 aagcctgact ctgttcattt caagcctgct tccagcaacc ccaagcccat cactggccac 1440  
 catgtctctg ctggcagcca ctccaagtct gccttcaatg ctgccaccag ccaccctaaa 1500  
 cccatcaagc cagctaccag ccatgctgag ccaccactg ctgactatcc caagcctgcc 1560  
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 tctagccctg ccgctgggcc caccaagcct gctgccagcc agctggagtc tgacaccatc 1740  
 gctgaccttc ctgaccctac tgtagtcaact accagtacca atgattacca tgatgtcgtg 1800  
 gttgttgatg ttgaagatga tcctgatgaa atggctgtgt ga 1842

<210> 142  
 <211> 613  
 <212> PRT  
 <213> Homo sapiens

<400> 142

Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys  
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Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe  
 20 25 30

Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met  
 35 40 45

Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn  
 50 55 60

Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr  
 65 70 75 80

Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu  
                     85                    90                    95

Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val  
                     100                    105                    110

Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys  
                     115                    120                    125

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn  
                     130                    135                    140

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
                     145                    150                    155                    160

Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr  
                     165                    170                    175

Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
                     180                    185                    190

Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr  
                     195                    200                    205

Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln  
                     210                    215                    220

Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe  
                     225                    230                    235                    240

Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu  
                     245                    250                    255

Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro  
                     260                    265                    270

Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys  
                     275                    280                    285

Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu  
                     290                    295                    300

Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Ser  
                     305                    310                    315                    320

Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala  
 325 330 335

Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala  
 340 345 350

His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
 355 360 365

Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
 370 375 380

His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala  
 385 390 395 400

Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
 405 410 415

His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
 420 425 430

Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala  
 435 440 445

Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
 450 455 460

Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
 465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr  
 485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
 500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
 515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro  
 530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
 545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu  
565 570

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser  
580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Asp Val Glu Asp Asp Pro  
595 600 605

Asp Glu Met Ala Val  
610

<210> 143  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 143  
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33

<210> 144  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 144  
ctccttcggt cctcctatcg ttgtcagaag t

31

<210> 145  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 145  
ttagatatcg gggcccaccc tagcgg

27

<210> 146  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 146  
ggtaccccca cagccatttc atcaggatc 29

<210> 147  
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<400> 147  
gatctggagt accccattga cgtcaatggg g 31

<210> 148  
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<400> 148  
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